SEQUENCE LISTING

<110> Vander Horn, Peter B.
        Wang, Yan
        MJ Bioworks, Incorporated

<120> Novel Compositions With Polymerase Activity

<130> 020130-001510US

<140> US 10/627,582
<141> 2003-07-25

<150> US 60/398,687
<151> 2002-07-25

<150> US 60/483,287
<151> 2003-06-27

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<170> PatentIn Ver. 2.1

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<223> Description of Artificial Sequence:full-length
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:full-length
      assembled hybrid polymerase clone Phy1

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Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
         35                  40                  45

Glu Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
     50                  55                  60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65                  70                  75                  80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
             85                  90                  95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
            100                 105                 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115                 120                 125

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130                 135                 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145                 150                 155                 160

Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
                165                 170                 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180                 185                 190

Arg Phe Leu Lys Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
        195                 200                 205
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2

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Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
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Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245             250                 255

His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
            260             265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
    275             280             285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Thr Gly Glu Gly
    290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
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Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
            325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
            355             360             365

Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Ala Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395             400

Ile Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Asn Tyr
            420             425             430

Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
    435             440             445

Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Lys Ile
    450             455             460

Lys Thr Lys Met Lys Ala Ser Gln Asp Pro Ile Glu Lys Ile Met Leu
465             470             475             480

Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
            515             520             525
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3

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Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
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Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
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Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
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Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
        675             680             685
Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
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Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705             710             715             720
Tyr Asp Pro Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735
Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
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Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ser
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PhS1, Phy1 and
      SSo7d fusion protein

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<212> PRT
<213> Artificial Sequence

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Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
        35   40   45

5

Glu Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65   70   75   80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
                85   90   95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
            100   105 .   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115   120   125

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
                165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180   185   190

Arg Phe Leu Lys Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
            195   200   205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210   215   220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245   250   255

His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
            260   265   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
    275   280   285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Thr Gly Glu Gly
    290   295   300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305   310   315   320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
            325   330   335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340   345   350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
            355   360   365

6

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Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Ala Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395                 400

Ile Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410                 415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Asn Tyr
            420             425             430

Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Lys Ile
    450             455             460

Lys Thr Lys Met Lys Ala Ser Gln Asp Pro Ile Glu Lys Ile Met Leu
465             470             475                 480

Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Lys
545             550             555                 560

Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
        580             585             590

Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635                 640

Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ser Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
        660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
        675             680             685
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7

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Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
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Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705                 710                 715                 720
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Tyr Asp Pro Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
                725                 730                 735
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Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
                740                 745                 750
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Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ser
            755                 760                 765
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Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
    770                 775                 780
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Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785                 790                 795                 800
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Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
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Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:hybrid
      polymerase Sso7d fusion protein PhS2

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8

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<210> 6
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Sso7d fusion protein PhS2

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 1               5                  10                  15


Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20                  25                  30


Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
        35                  40                  45


Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
    50                  55                  60


Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Lys Pro Ile
65                  70                  75                  80


Glu Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
                85                  90                  95


Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
            100                 105                 110


Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115                 120                 125


Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
    130                 135                 140
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9

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
               165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
          180   185   190

Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
          195   200   205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
     210   215   220

Lys Leu Gly Ile Lys Leu Pro Ile Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
          245   250   255

His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
          260   265   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
          275   280   285

Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Ser Gly Glu Gly
     290   295   300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305   310   315   320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ile Gln Leu Ser Arg Leu
               325   330   335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
          340   345   350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
          355   360   365

Pro Asn Lys Pro Ser Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
     370   375   380

Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385   390   395   400

Ile Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
          405   410   415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Glu Tyr
          420   425   430

Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
          435   440   445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
     450   455   460

10

Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Ile Leu Leu
465   470   475   480

Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
              485   490   495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
          500   505   510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Arg Lys Glu
          515   520   525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530   535   540

Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Lys
545   550   555   560

Ala Leu Glu Phe Val Asp Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
              565   570   575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
          580   585   590

Lys Arg Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
          595   600   605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610   615   620

Ala Lys Val Leu Glu Thr Ile Leu Lys His Gly Asn Val Glu Glu Ala
625   630   635   640

Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
              645   650   655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Pro Pro Leu His
          660   665   670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
          675   680   685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690   695   700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705   710   715   720

Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
              725   730   735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
          740   745   750

Lys Glu Asp Leu Arg Tyr Gln Lys Thr Lys Gln Val Asp Leu Thr Ala
          755   760   765

Cys Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
    770   775   780

11

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785   790   795   800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
              805   810   815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
              820   825   830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
          835   840

<210> 7
<211> 2535
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Sso7d fusion protein PhS5

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ctgctgagag atgattctca gattgatgaa gttaaaaaaa tcactgctga gcgccatggc 180
aagattgttc gtatcattga tgcggaaaag gtagaaaaga aatttctggg cagaccaatc 240
accgtgtgga gactgtattt cgaacatcca caagatgttc cggctattcg cgataaagtt 300
cgcgaacatc ctgcagttgt tgacatcttc gaatacgata ttccatttgc aaagcgttac 360
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gatatagaaa ccctctatca cgaaggcgaa gagtttggta aaggcccaat tataatgatc 480
agctatgcag atgaaaacga agcaaaggtg attacttgga aaaaaatagg tctcccatac 540
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aaggatccgg acattatcat tacttataac ggcgactctt ttgacttccc atatctggcg 660
aaacgcgcag aaaaactcgg tattaaactg cctctcggcc gtgatggttc cgagccgaag 720
atgcagcgta tcggcgatat gaccgctgta gaaattaagg tcgtatcca tttcgacctg 780
tatcatgtaa ttactcgtac tattaacctc ccgacttaca ctctcgaggc tgtatatgaa 840
gcaatttttg gtaagccgaa ggagaaggta tacgccgatg agattgcaga ggcgtgggaa 900
tccggtaaga acctcgagcg tgttgcaaaa tactccatgg aagatgcaaa ggcgacttat 960
gaactcggca agaattcct cccaatggaa atccagctct ctcgcctggt tggccaacca 1020
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gcgtacgaac gcaacgaagt ggctccgaac aagccagacg aagaagagta tgaacgccgt 1140
ctccgcgagt cttacactgg tggctatgtt aaagagccag aaaagggcct ctgggaaaac 1200
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ccggatactc tcaaccgcga gggctgcaaa gagtatgata ttgctccgca agtaggccac 1320
aagttctgca aggacttccc gggctttatt ccgtctctcc tgaaacatct gctcgatgaa 1380
cgccaagaga ttaagcgtaa aatgaaggcg tccaaggatc cgattgaaaa aaaaatgctc 1440
gactatcgcc aaagagcgat taaactcctc gcaaactctt tttacggcta ttatggctat 1500
gcaaaagcac gctggtactg taaggagtgt gctgagtccg ttactgcttg gggtcgcgaa 1560
tacatcgagc tcgtgtggaa ggagctcgaa gaaaagtttg gctttaaagt tctctacatt 1620
gacactgatg gtctctatgc gactattccg ggtggtaagc ctgaggaaat taagaaaaag 1680
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gcggtactcc gtattctgga ggcttttggc taccgtaagg aagacctccg ctggcaaaag 2280

12

actaaacagg ttggcctcac ttcttggctc aacattaaaa aatccggtac cggcggtggc 2340
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aagaaagtat ggcgtgtggg caagatgatc tccttcacct acgacgaggg cggtggcaag 2460
accggccgtg gtgcggtaag cgaaaaggac gcgccgaagg agctgctgca gatgctggag 2520
aagcagaaaa agtga 2535

<210> 8
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Sso7d fusion protein PhS5

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  1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
                20   25   30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
            35   40   45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
        50   55   60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65   70   75   80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
                85   90   95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
        130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
                165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180   185   190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
            195   200   205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
        210   215   220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

13

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
                245   250   255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
                260   265   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
                275   280   285

Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn
        290   295   300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305   310   315   320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
                325   330   335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
                340   345   350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
                355   360   365

Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
        370   375   380

Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385   390   395   400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
                405   410   415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr
                420   425   430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
        435   440   445

Phe Ile Pro Ser Leu Leu Lys His Leu Leu Asp Glu Arg Gln Glu Ile
        450   455   460

Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu
465   470   475   480

Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
                485   490   495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
                500   505   510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Trp Lys Glu
                515   520   525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
        530   535   540

Leu Tyr Ala Thr Ile Pro Gly Gly Lys Pro Glu Glu Ile Lys Lys Lys
545   550   555   560

14

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Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
                565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
        675             680             685

Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser
            755             760             765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
    770             775             780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785             790             795             800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
            805             810             815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
        820             825             830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
        835             840


<210> 9
<211> 2535
<212> DNA
<213> Artificial Sequence
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15

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Sso7d fusion protein PhS7

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ctgctgagag atgattctca gattgatgaa gttaaaaaaa tcactgctga gcgccatggc 180
aagattgttc gtatcattga tgcggaaaag gtagaaaaga aatttctggg cagaccaatc 240
accgtgtgga gactgtattt cgaacatcca caagatgttc cggctattcg cgataaagtt 300
cgcgaacatc ctgcagttgt tgacatcttc gaatacgata ttccatttgc aaagcgttac 360
ctcatcgaca aaggcctgat accaatggag ggcgaggaag aactcaagct cctggcgttc 420
gatatagaaa ccctctatca cgaaggcgaa gagtttggta aaggcccaat tataatgatc 480
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ctcgcgattt atgagcagat tactcgcccg ctgcatgagt ataaggcgat tggtccgcac 2040
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aagaaagtat ggcgtgtggg caagatgatc tccttcacct acgacgaggg cggtggcaag 2460
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aagcagaaaa agtga 2535

<210> 10
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Sso7d fusion protein PhS7

16

<400> 10

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Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
             20                  25                  30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
         35                  40                  45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
     50                  55                  60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65                  70                  75                  80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
             85                  90                  95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
             100                 105                 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
         115                 120                 125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
     130                 135                 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145                 150                 155                 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
             165                 170                 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
             180                 185                 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
             195                 200                 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
     210                 215                 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225                 230                 235                 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
             245                 250                 255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
             260                 265                 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
         275                 280                 285

Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn
     290                 295                 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305                 310                 315                 320
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17

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Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
            325                 330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
        355             360             365

Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395                 400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Asn Tyr
            420             425             430

Asp Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Gly Arg Leu Leu Glu Glu Arg Gln Glu Ile
    450             455             460

Lys Thr Lys Met Lys Ala Thr Lys Asp Pro Ile Glu Lys Lys Leu Leu
465             470             475                 .480

Asp Tyr Arg Gln Lys Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500             505             510

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Phe Val Arg Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Lys Pro Glu Glu Ile Lys Lys Lys
545             550             555                 560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635                 640
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18

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Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
                645                 650                 655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
                660                 665                 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
                675                 680                 685

Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
    690                 695                 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705                 710                 715                 720

Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
                725                 730                 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
                740                 745                 750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser
                755                 760                 765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
    770                 775                 780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785                 790                 795                 800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
                805                 810                 815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
                820                 825                 830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
        835                 840


<210> 11
<211> 2337
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Hyb1

<220>
<221> modified_base
<222> (1416)
<223> n = g, a, c or t

<400> 11
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ctgctgagag atgattctaa gattgaggaa gttagaaaaa tcactgctga gcgccatggc 180
aagattgttc gtatcgttga tgtggaaaag gtaaggaaga aatttctggg cagaccaatc 240
aaggtgtgga gactgtattt cgaacatcca caagatgttc gactattcg cgataaagtt 300
cgcgaacatc ctgcagttat tgacatcttc gaatacgata ttgcatttgc aaagcgttac 360
```

19

```
ctcatcgaca aaggcctgat accaatggag ggcgaggaag aactcaagat cctggcgttc 420
gatatagaaa ccctctatca cggaagcgaa gagtttggta aaggcccaat tataatgatc 480
agctatgcag atgaaaacga agcaaaggtg attacttgga aaaacataga tctcccatac 540
gttgaggttg tatcttccga gcgcgagatg attaaacgct ttctcagaat tatccgcgag 600
aaggatccgg acattatcgt tacttataac ggcgactctt ttgacctccc atatctggcg 660
aaacgcgcag aaaaactcgg tattaaactg actctcggcc gtgatggttg cgaggcgaag 720
atgcagcgtc tcggcgatat gaccgctgta gaagttaagg gtcgtatcca tttcgacctg 780
tattatgtaa ttagccgtac tattaacctc ccgacttaca ctctcgaggc tgtatatgaa 840
gcaatttttg gtaagccgaa ggagaaggta tacgccgatg atattgcaga ggcgtgggaa 900
accggtaagg gcctcgagcg tgttgcaaaa tactccatgg aagatgcaaa ggcgacttat 960
gaactcggca aagaattcct cccaatggaa gctcagctct ctcgcctggt tggccaacca 1020
ctgtgggatg tttctcgttc ttccaccggt aacctcgtag agtggtatct cctgcgcaaa 1080
gcgtacgaac gcaacgaagt ggctccgaac aagccatacg aacgagagta tgaacgccgt 1140
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aagttctgca aggacttcct tggctttatt ccgtctctcc tggggcatct gctcgaggaa 1380
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gactatcgcc aaaaagcgat taaactcctc gcaaactctt attacggcta ttatggctat 1500
gcaaaagcac gctggtactg taaggagtgt gctgagtccg ttactgcttg gggtcgcgaa 1560
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gaaggcaaaa ttattactcg tggtctcgag attgtgcgcc gtgattggag cgaaattgcg 1860
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gtgaaaattg taaaagaaat aatcgaaaag ctcgctaaat atgaaatacc gccagagaag 1980
ctcgcgattt atgagcagat tactcgcccg ctgcatgagt ataaggcgat tggtccgcac 2040
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ggctacattg tactccgcgg cgatggtccg attagcaaac gtgcaattct agctgaggaa 2160
ttcgatccga aaaagcacaa gtatgacgca gaatattaca ttgagaacca ggtgctcccg 2220
gcggtactcc gtattctgga gggttttggc taccgtaagg aagacctccg ttggcaaaag 2280
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```


<210> 12
<211> 775
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Hyb1

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 12
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 1               5                  10                  15


Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg
            20                  25                  30


Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
        35                  40                  45


Glu Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50                  55                  60
```

20

```
Ile Val Asp Val Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
65              70              75                      80

Lys Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
            85              90                      95

Arg Asp Lys Val Arg Glu His Pro Ala Val Ile Asp Ile Phe Glu Tyr
            100             105 .                 110

Asp Ile Ala Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115             120             125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
    130             135             140

Leu Tyr His Gly Ser Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145             150             155                     160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
            165             170                     175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
        180             185             190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
        195             200             205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210             215             220

Lys Leu Gly Ile Lys Leu Thr Leu Gly Arg Asp Gly Cys Glu Ala Lys
225             230             235                     240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245             250                     255

His Phe Asp Leu Tyr Tyr Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
        260             265             -   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
    275             280             285

Lys Val Tyr Ala Asp Asp Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
    290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315                     320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ala Gln Leu Ser Arg Leu
            325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
            355             360             365

Pro Asn Lys Pro Tyr Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380
```

21

```
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Ser
385             390             395             400

Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420             425             430

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
    450             455             460

Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
        580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
        660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675             680             685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700
```

22

Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
705   710   715   720

Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
                725   730   735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740   745   750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
        755   760   765

Trp Leu Asn Ile Lys Lys Ser
    770   775

<210> 13
<211> 2535
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Hyb1-Sso7d fusion protein HyS1

<220>
<221> modified_base
<222> (1416)
<223> n = g, a, c or t

<400> 13
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ctgctgagag atgattctaa gattgaggaa gttagaaaaa tcactgctga gcgccatggc 180
aagattgttc gtatcgttga tgtggaaaag gtaaggaaga aatttctggg cagaccaatc 240
aaggtgtgga gactgtattt cgaacatcca caagatgttc cgactattcg cgataaagtt 300
cgcgaacatc ctgcagttat tgacatcttc gaatacgata ttgcatttgc aaagcgttac 360
ctcatcgaca aaggcctgat accaatggag ggcgaggaag aactcaagat cctggcgttc 420
gatatagaaa ccctctatca cggaagcgaa gagtttggta aaggcccaat tataatgatc 480
agctatgcag atgaaaacga agcaaaggtg attacttgga aaaacataga tctcccatac 540
gttgaggttg tatcttccga cgcgcgagatg attaaacgct ttctcagaat tatccgcgag 600
aaggatccgg acattatcgt tacttataac ggcgactctt ttgacctccc atatctggcg 660
aaacgcgcag aaaaactcgg tattaaactg actctcggcc gtgatggttg cgaggcgaag 720
atgcagcgtc tcggcgatat gaccgctgta gaagttaagg gtcgtatcca tttcgacctg 780
tattatgtaa ttagccgtac tattaacctc ccgacttaca ctctcgaggc tgtatatgaa 840
gcaattttg gtaagccgaa ggagaaggta tacgccgatg atattgcaga ggcgtgggaa 900
accggtaagg gcctcgagcg tgttgcaaaa tactccatgg aagatgcaaa ggcgacttat 960
gaactcggca agaattcct cccaatggaa gctcagctct tcgcctggt tggccaacca 1020
ctgtgggatg tttctcgttc ttccaccggt aacctcgtag agtggtatct cctgcgcaaa 1080
gcgtacgaac gcaacgaagt ggctccgaac aagccatacg aacgagagta tgaacgccgt 1140
ctccgcgagt cttacactgg tggctttgtt aaagagccag aaaagggcct ctgggaaagc 1200
ctcgtgtccc tcgatttcg ctctctgtat ccgtctatta tcattaccca aacgtgtct 1260
ccggatactc tcaaccgcga gggctgcaaa gactatgata ttgctccgga agtaggccac 1320
aagttctgca aggacttcct ggctttatt ccgtctctcc tggggcatct gctcgaggaa 1380
cgccaagaga ttaagaccaa aatgaaggag acccangatc cgattgaaaa aatactgctc 1440
gactatcgcc aaaaagcgat taaactcctc gcaaactctt attacggcta ttatggctat 1500
gcaaaagcac gctggtactg taaggagtgt gctgagtccg ttactgcttg gggtcgcgaa 1560
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gacactgatg gtctctatgc gactattccg ggtggtgagc tgaggaaat taagaaaaag 1680
gctctagaat ttgtgaaata cattaactcg aagctccccg gtctcttgga gctcgaatat 1740
gaaggctttt ataagcgcgg cttcttcgtt accaagaaga gatatgcggt gattgatgaa 1800

23

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gaaggcaaaa ttattactcg tggtctcgag attgtgcgcc gtgattggag cgaaattgcg 1860
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gtgaaaattg taaaagaaat aatcgaaaag ctcgctaaat atgaaatacc gccagagaag 1980
ctcgcgattt atgagcagat tactcgcccg ctgcatgagt ataaggcgat tggtccgcac 2040
gtggctgttg caaagaaact ggctgctaga ggcgtgaaaa ttaaaccggg tatggtaatt 2100
ggctacattg tactccgcgg cgatggtccg attagcaaac gtgcaattct agctgaggaa 2160
ttcgatccga aaaagcacaa gtatgacgca gaatattaca ttgagaacca ggtgctcccg 2220
gcggtactcc gtattctgga gggttttggc taccgtaagg aagacctccg ttggcaaaag 2280
actaaacagg ctggcctcac tgcttggctc aacattaaaa aatccggtac cggcggtggc 2340
ggtgcaaccg taaagttcaa gtacaaaggc gaagaaaaag aggtagacat ctccaagatc 2400
aagaaagtat ggcgtgtggg caagatgatc tccttcacct acgacgaggg cggtggcaag 2460
accggccgtg gtgcggtaag cgaaaaggac gcgccgaagg agctgctgca gatgctggag 2520
aagcagaaaa agtga                                                   2535


<210> 14
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Hyb1-Sso7d fusion protein HyS1

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 14
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile
  1               5                  10                  15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg
                 20                  25                  30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
             35                  40                  45

Glu Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
         50                  55                  60

Ile Val Asp Val Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
 65                  70                  75                  80

Lys Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
                 85                  90                  95

Arg Asp Lys Val Arg Glu His Pro Ala Val Ile Asp Ile Phe Glu Tyr
                100                 105                 110

Asp Ile Ala Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115                 120                 125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
        130                 135                 140

Leu Tyr His Gly Ser Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145                 150                 155                 160
```

24

```
Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
            165                 170             175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180                 185             190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
            195                 200             205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210                 215             220

Lys Leu Gly Ile Lys Leu Thr Leu Gly Arg Asp Gly Cys Glu Ala Lys
225                 230             235             240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245             250             255

His Phe Asp Leu Tyr Tyr Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
            260             265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
    275             280             285

Lys Val Tyr Ala Asp Asp Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
    290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315             320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ala Gln Leu Ser Arg Leu
            325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
            355             360             365

Pro Asn Lys Pro Tyr Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Ser
385             390             395             400

Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420             425             430

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
    450             455             460

Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480
```

25

```
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
            515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
            595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
            675             680             685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
            755             760             765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
    770             775             780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785             790             795             800
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Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
              805                   810                 815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
              820                   825                 830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
          835                   840


<210> 15
<211> 2340
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:truncated
      hybrid polymerase Hyb2

<220>
<221> modified_base
<222> (1416)
<223> n = g, a, c or t

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ctgctggaag atgattctaa gattgatgaa gttagaaaaa tcactgctga gcgccatggc 180
aagattgttc gtatcgttga tgcggaaaag gtagagaaga aatttctggg cagaccaatc 240
acggtgtgga aactgtattt cgaacatcca caagatgttc cgactattcg cgagaaaatt 300
cgcgaacatt ctgcagttgt tggcatcttc gaatacgata ttccatttgc aaagagttac 360
ctcatcgaca aaggcctgat accaatggag ggcgaggaag aactcaagct cctggcgttc 420
gatatagaaa ccctctatca cgaaggcgaa gagtttgcta aaggcccaat tataatgatc 480
agctatgcag atgaagacga agcaaaggtg attacttgga aaaaaataga tctcccatac 540
gttgaggttg tatcttccga gcgcgagatg attaagcgct ttctcagagt tatccgcgag 600
aaggatccgg acgttatcgt tacttataac ggcgactctt ttgacctccc atatctggcg 660
aaacgcgcag aaaaactcgg tattaaactg cctctcggcc gtgatggttc cgagccgaag 720
atgcagcgtc tcggcgatat gaccgctgta gaagttaagg tcgtatcca tttcgacctg 780
tatcatgtaa ttagccgtac tattaacctc ccgacttaca ctctcgaggc tgtatatgaa 840
gcaatttttg gtaagccgaa ggagaaggta tacgccgatg agattgcagg ggcgtgggaa 900
accggtgagg acctcgagcg tgttgcaaaa tactccatgg aagatgcaaa ggcgatttat 960
gaactcggca agaattctt cccaatggaa gttcagctcc ctcgcctggt tggccaacca 1020
ctgtgggatg tttctcgttc ttccaccggt aacctcgtag agtggttgct cctgcgcaaa 1080
gcgtacgaac gcaacgaact ggctccgaac aagccagccg aacaagagta tgaacgccgt 1140
ctccgcgagt cttacactgg tggctttgtt aaagagccag aaaagggcct ctgggaagac 1200
ctcgtgtccc tcgattttcg cgctctgtat ccgtctatta tcattaccca aacgtgtct 1260
ccggatactc tcaaccgcga gggctgcaaa gactatgata ttgctccgga agtaggccac 1320
aagttctgca aggacttcct tggctttatt ccgtctctcc tggggcatct gctcgaggaa 1380
cgccaagaga ttaagaccaa aatgaaggag acccangatc cgattgaaaa aatactgctc 1440
gactatcgcc aaaaagcgat taaactcctc gcaaactctt attacggcta ttatggctat 1500
gcaaaagcac gctggtactg taaggagtgt gctgagtccg ttactgcttg gggtcgcgaa 1560
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gacactgatg gtctctatgc gactattccg ggtggtgagc ctgaggaaat taagaaaaag 1680
gctctagaat ttgtgaaata cattaactcg aagctcccg gtctcttgga gctcgaatat 1740
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gaaggcaaaa ttattactcg tggtctcgag attgtgcgcc gtgattggag cgaaattgcg 1860
aaagaaactc aagctaaagt ctcgaggct attctcaaac acggcaacgt tgaagaagct 1920
gtgaaaattg taaaagaaat aatcgaaaag ctcgctaaat atgaaatacc gccagagaag 1980
ctcgcgattt atgagcagat tactcgcccg ctgcatgagt ataaggcgat tggtccgcac 2040
gtggctgttg caaagaaact ggctgctaga ggcgtgaaaa ttaaaccggg tatggtaatt 2100
ggctacattg tactccgcgg cgatggtccg attagcaacc gtgcaattct agctgaggaa 2160
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27

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ttcgatctga gaaagcacaa gtatgacgca gaatattaca ttgagaacca ggtgctcccg 2220
gcggtactcc gtattctgga gggttttggc taccgtaagg aagacctccg ttagcaaaag 2280
actaaacagg ctggactcac tgcttggctc atcattaaaa aatccggtac ccactagtgc 2340
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<210> 16
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:truncated
      hybrid polymerase Hyb2

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 16

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Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1               5                  10                  15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
                20                  25                  30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
            35                  40                  45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
        50                  55                  60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65                  70                  75                  80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
                85                  90                  95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
               100                 105                 110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
           115                 120                 125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
       130                 135                 140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145                 150                 155                 160

Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
               165                 170                 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
           180                 185                 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
           195                 200                 205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
       210                 215                 220
```

```
Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235                     240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245             250             255

His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
            260             265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275             280             285

Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
        290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
305             310             315             320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
            325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
            355             360             365

Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
385             390             395             400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420             425             430

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
    450             455             460

Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540
```

29

```
Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545             550         555         560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
                565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675             680             685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg
        755


<210> 17
<211> 2340
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:truncated
      hybrid polymerase Hyb3

<220>
<221> modified_base
<222> (1416)
<223> n = g, a, c or t

<400> 17
atgatcctgg atgctgacta catcactgaa gaaggcaaac cggttatccg tatcttcaaa 60
aaagagaacg gcgaatttaa ggttgagtat gatcgcaact ttcgtccata catttacgct 120
ctgctggaag atgattctaa gattgatgaa gttagaaaaa tcactgctga gcgccatggc 180
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aagattgttc gtatcgttga tgcggaaaag gtagagaaga aatttctggg cagaccaatc 240
acggtgtgga aactgtattt cgaacatcca caagatgttc cgactattcg cgagaaaatt 300
cgcgaacatt ctgcagttgt tggcatcttc gaatacgata ttccatttgc aaagagttac 360
ctcatcgaca aaggcctgat accaatggag ggcgaggaag aactcaagct cctggcgttc 420
gatatagaaa ccctctatca cgaaggcgaa gagtttgcta aaggcccaat tataatgatc 480
agctatgcag atgaagacga agcaaaggtg attacttgga aaaaaataga tctcccatac 540
gttgaggttg tatcttccga gcgcgagatg attaagcgct ttctcagagt tatccgcgag 600
aaggatccgg acgttatcgt tacttataac ggcgactctt ttgacctccc atatctggcg 660
aaacgcgcag aaaaactcgg tattaaactg cctctcggcc gtgatggttc cgagccgaag 720
atgcagcgtc tcggcgatat gaccgctgta gaagttaagg gtcgtatcca tttcgacctg 780
tatcatgtaa ttagccgtac tattaacctc ccgacttaca ctctcgaggc tgtatatgaa 840
gcaatttttg gtaagccgaa ggagaaggta tacgccgatg agattgcagg ggcgtgggaa 900
accggtgagg acctcgagcg tgttgcaaaa tactccatgg aagatgcaaa ggcgatttat 960
gaactcggca aagaattctt cccaatggaa gttcagctcc ctcgcctggt tggccaacca 1020
ctgtgggatg tttctcgttc ttccaccggt aacctcgtag agtggttgct cctgcgcaaa 1080
gcgtacgaac gcaacgaact ggctccgaac aagccagccg aacaagagta tgaacgccgt 1140
ctccgcgagt cttacactgg tggctttgtt aaagagccag aaaagggcct ctgggaagac 1200
ctcgtgtccc tcgattttcg cgctctgtat ccgtctatta tcattaccca caacgtgtct 1260
ccggatactc tcaaccgcga gggctgcaaa gactatgata ttgctccgga agtaggccac 1320
aagttctgca aggacttcct tggctttatt ccgtctctcc tggggcatct gctcgaggaa 1380
cgccaagaga ttaagaccaa aatgaaggag acccangatc cgattgaaaa aatactgctc 1440
gactatcgcc aaaaagcgat taaactcctc gcaaactctt attacggcta ttatggctat 1500
gcaaaagcac gctggtactg taaggagtgt gctgagtccg ttactgcttg gggtcgcgaa 1560
tacatcgagt tcgtgtggaa ggagctcgaa gaaaagtttg gctttaaagt tctctacatt 1620
gacactgatg gtctctatgc gactattccg ggtggtgagc ctgaggaaat taagaaaaag 1680
gctctagaat ttgtgaaata cattaactcg aagctccccg gtctcttgga gctcgaatat 1740
gaaggctttt ataagcgcgg cttcttcgtt accaagaaga gatatgcggt gattgatgaa 1800
gaaggcaaaa ttattactcg tggtctcgag attgtgcgcc gtgattggag cgaaattgcg 1860
aaagaaactc aagctaaagt tctcgaggct attctcaaac acggcaacgt tgaagaagct 1920
gtgaaaattg taaagaaat aatcgaaaag ctcgctaaat atgaaatacc gccagagaag 1980
ctcgcgattt atgagcagat tactcgcccg ctgcatgagt ataaggcgat tggtccgcac 2040
gtggctgttg caaagaaact ggctgctaga ggcgtgaaaa ttaaaccggg tatggtaatt 2100
ggctacattg tactccgcgg cgatggtccg attagcaacc gtgcaattct agctgaggaa 2160
ttcgatctga gaaagcacaa gtatgacgca gaatattaca ttgagaacca ggtgctcccg 2220
gcggtactcc gtattctgga gggttttggc taccgtaagg aagacctccg ttagcaaaag 2280
actaaacagg ctggactcac tgcttggctc atcattaaaa aatccggtac ccactagtgc 2340
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<210> 18
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:truncated
      hybrid polymerase Hyb3

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 18
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1   5   10   15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
             20   25   30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
         35   40   45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
   50   55   60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65   70   75   80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
          85   90   95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
        100   105   110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
        130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
        165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
        180   185   190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
        195   200   205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
        210   215   220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
        245   250   255

His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
        260   265   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275   280   285

Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
        290   295   300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
305   310   315   320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
        325   330   335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
        340   345   350

Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
        355   360   365

```
Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
385             390             395             400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420             425             430

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
    450             455             460

Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
        580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675             680             685
```

33

```
Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695         700
```

```
Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
    705             710         715             720
```

```
Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
                725             730             735
```

```
Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
                740             745             750
```

```
Lys Glu Asp Leu Arg
        755
```

<210> 19
<211> 2535
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Sso7d fusion protein HyS4

<220>
<221> modified_base
<222> (1416)
<223> n = g, a, c or t

<400> 19
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aaagagaacg gcgaatttaa ggttgagtat gatcgcaact ttcgtccata catttacgct 120
ctgctggaag atgattctaa gattgatgaa gttagaaaaa tcactgctga gcgccatggc 180
aagattgttc gtatcgttga tgcggaaaag gtagagaaga aatttctggg cagaccaatc 240
acggtgtgga aactgtattt cgaacatcca caagatgttc cgactattcg cgagaaaatt 300
cgcgaacatt ctgcagttgt tggcatcttc gaatacgata ttccatttgc aaagagttac 360
ctcatcgaca aaggcctgat accaatggag ggcgaggaag aactcaagct cctggcgttc 420
gatatagaaa ccctctatca cgaaggcgaa gagtttgcta aaggcccaat tataatgatc 480
agctatgcag atgaagacga agcaaaggtg attacttgga aaaaaataga tctcccatac 540
gttgaggttg tatcttccga gcgcgagatg attaagcgct ttctcagagt tatccgcgag 600
aaggatccgg acgttatcgt tacttataac ggcgactctt ttgacctccc atatctggcg 660
aaacgcgcag aaaaactcgg tattaaactg cctctcggcc gtgatggttc cgagccgaag 720
atgcagcgtc tcggcgatat gaccgctgta gaagttaagg gtcgtatcca tttcgacctg 780
tatcatgtaa ttagccgtac tattaacctc ccgacttaca ctctcgaggc tgtatatgaa 840
gcaatttttg gtaagccgaa ggagaaggta tacgccgatg agattgcagg ggcgtgggaa 900
accggtgagg acctcgagcg tgttgcaaaa tactccatgg aagatgcaaa ggcgatttat 960
gaactcggca agaattctt cccaatggaa gttcagctcc ctcgcctggt tggccaacca 1020
ctgtgggatg tttctcgttc ttccaccggt aacctcgtag agtggttgct cctgcgcaaa 1080
gcgtacgaac gcaacgaact ggctccgaac aagccagccg aacaagagta tgaacgccgt 1140
ctccgcgagt cttacactgg tggctttgtt aaagagccag aaaagggcct ctgggaagac 1200
ctcgtgtccc tcgattttcg cgctctgtat ccgtctatta tcattaccca caacgtgtct 1260
ccggatactc tcaaccgcga gggctgcaaa gactatgata ttgctccgga agtaggccac 1320
aagttctgca aggacttcct tggctttatt ccgtctctcc tggggcatct gctcgaggaa 1380
cgccaagaga ttaagaccaa aatgaaggag acccangatc cgattgaaaa aatactgctc 1440
gactatgcc aaaaagcgat taaactcctc gcaaactctt attacggcta ttatggctat 1500
gcaaaagcac gctggtactg taaggagtgt gctgagtccg ttactgcttg gggtcgcgaa 1560
tacatcgagt tcgtgtggaa ggagctcgaa gaaaagtttg gctttaaagt tctctacatt 1620
gacactgatg gtctctatgc gactattccg ggtggtgagc tgaggaaat taagaaaaag 1680
gctctagaat ttgtgaaata cattaactcg aagctccccg gtctcttgga gctcgaatat 1740
gaaggctttt ataagcgcgg cttcttcgtt accaagaaga gatatgcggt gattgatgaa 1800
```

34

```
gaaggcaaaa ttattactcg tggtctcgag attgtgcgcc gtgattggag cgaaattgcg 1860
aaagaaactc aagctaaagt tctcgaggct attctcaaac acggcaacgt tgaagaagct 1920
gtgaaaattg taaagaaat aatcgaaaag ctcgctaaat atgaaatacc gccagagaag 1980
ctcgcgattt atgagcagat tactcgcccg ctgcatgagt ataaggcgat tggtccgcac 2040
gtggctgttg caaagaaact ggctgctaga ggcgtgaaaa ttaaaccggg tatggtaatt 2100
ggctacattg tactccgcgg cgatggtccg attagcaaac gtgcaattct agctgaggaa 2160
ttcgatccga aaaagcacaa gtatgacgca gaatattaca ttgagaacca ggtgctcccg 2220
gcggtactcc gtattctgga gggttttggc taccgtaagg aagacctccg ttggcaaaag 2280
actaaacagg ctggcctcac tgcttggctc aacattaaaa aatccggtac cggcggtggc 2340
ggtgcaaccg taaagttcaa gtacaaaggc gaagaaaaag aggtagacat ctccaagatc 2400
aagaaagtat ggcgtgtggg caagatgatc tccttcacct acgacgaggg cggtggcaag 2460
accggccgtg gtgcggtaag cgaaaaggac gcgccgaagg agctgctgca gatgctggag 2520
aagcagaaaa agtga                                                   2535


<210> 20
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
     polymerase Sso7d fusion protein HyS4

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 20
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1               5                  10                  15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
             20                  25                  30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
         35                  40                  45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
     50                  55                  60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65                  70                  75                  80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
                 85                  90                  95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
             100                 105                 110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
         115                 120                 125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
     130                 135                 140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145                 150                 155                 160
```

35

```
Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
            165                     170             175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180                 185             190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
            195                 200             205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210                 215             220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225                 230             235                 240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245                 250             255

His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
            260                 265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275                 280             285

Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
    290                 295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
305                 310             315                 320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
            325                 330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340                 345             350

Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
        355                 360             365

Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370                 375             380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
385                 390             395                 400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405                 410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420                 425             430

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
        435                 440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
    450                 455             460

Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465                 470             475                 480
```

36

```
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
            515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675             680             685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
            755             760             765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
    770             775             780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785             790             795             800
```

37

```
Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
            805                 810                 815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
            820                 825                 830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
        835                 840


<210> 21
<211> 189
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Sso7d coding
      region

<400> 21
accgtaaagt tcaagtacaa aggcgaagaa aaagaggtag acatctccaa gatcaagaaa 60
gtatggcgtg tgggcaagat gatctccttc acctacgacg agggcggtgg caagaccggc 120
cgtggtgcgg taagcgaaaa ggacgcgccg aaggagctgc tgcagatgct ggagaagcag 180
aaaaagtga                                                        189


<210> 22
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Sso7d binding
      domain

<400> 22
Ala Thr Val Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile
  1               5                  10                  15

Ser Lys Ile Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr
            20                  25                  30

Tyr Asp Glu Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys
            35                  40                  45

Asp Ala Pro Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
    50                  55                  60


<210> 23
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:signature
      invariable sequence element in hybrid polymerases
      containing nucleotide binding motif
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<400> 23
Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys
 1   5   10   15

Ala Glu Ser Val Thr Ala Trp Gly Arg
            20   25

<210> 24
<211> 775
<212> PRT
<213> Pyrococcus furiosus

<220>
<223> parent Pyrococcus furiosus family B DNA
      polymerase PolI (Pfu)

<400> 24
Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
            20   25   30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
        35   40   45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65   70   75   80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
            85   90   95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
            165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
        180   185   190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
        195   200   205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
    210   215   220

39

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
               245   250   255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
               260   265   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
           275   280   285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
    290   295   300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305   310   315   320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
               325   330   335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
               340   345   350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
           355   360   365

Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
    370   375   380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385   390   395   400

Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
               405   410   415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
               420   425   430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
           435   440   445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
    450   455   460

Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465   470   475   480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
           485   490   495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
           500   505   510

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
           515   520   525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530   535   540

40

```
Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
                565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
625             630             635             640

Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675             680             685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
            755             760             765

Trp Leu Asn Ile Lys Lys Ser
    770             775


<210> 25
<211> 775
<212> PRT
<213> Pyrococcus sp.

<220>
<223> parent Pyrococcus sp. strain GD-B PolI
      (Deep Vent) DNA polymerase

<400> 25
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
 1               5               10              15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20              25              30
```

```
Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Gln Ile
         35              40              45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
     50              55              60

Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
 65              70              75              80

Glu Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
             85              90              95

Arg Asp Lys Ile Arg Glu His Ser Ala Val Ile Asp Ile Phe Glu Tyr
             100             105             110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
         115             120             125

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
     130             135             140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145             150             155             160

Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
             165             170             175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
         180             185             190

Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Val Ile Ile Thr
         195             200             205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Val Lys Arg Ala Glu
     210             215             220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235             240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
             245             250             255

His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
             260             265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
         275             280             285

Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
     290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
305             310             315             320

Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
             325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
         340             345             350
```

42

```
Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
        355                 360                 365

Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
        370                 375                 380

Tyr Ala Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Gly
385                 390                 395                 400

Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
                405                 410                 415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Glu Tyr
                420                 425                 430

Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
            435     .           440                 445

Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Glu Ile
        450                 455                 460

Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu
465                 470                 475                 480

Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
                485                 490                 495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500                 505                 510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu
            515                 520                 525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
        530                 535                 540

Leu Tyr Ala Thr Ile Pro Gly Ala Lys Pro Glu Glu Ile Lys Lys Lys
545                 550                 555                 560

Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu
                565                 570                 575

Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
            580                 585                 590

Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
            595                 600                 605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
        610                 615                 620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625                 630                 635                 640

Val Lys Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Ile
                645                 650                 655

Pro Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
        660                 665                 670
```

43

```
Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
        675             680             685

Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
        690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
                725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ala
            755             760             765

Trp Leu Asn Ile Lys Lys Lys
    770             775


<210> 26
<211> 775
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:designed hybrid
      polymerase

<220>
<221> MOD_RES
<222> (1)..(775)
<223> Xaa = unknown amino acid

<400> 26
Met Ile Leu Asp Xaa Asp Tyr Ile Thr Glu Xaa Gly Lys Pro Xaa Ile
  1             5               10              15

Arg Xaa Phe Lys Lys Glu Asn Gly Xaa Phe Lys Xaa Glu Xaa Asp Arg
            20              25              30

Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile
        35              40              45

Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg
    50              55              60

Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile
65              70              75              80

Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile
            85              90              95

Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr
        100             105             110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115             120             125
```

44

Met Glu Gly Xaa Glu Glu Leu Lys Xaa Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Xaa Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Xaa Glu Ala Lys Val Ile Thr Trp Lys Xaa Ile
                165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180   185   190

Arg Phe Leu Xaa Xaa Ile Arg Glu Lys Asp Pro Asp Xaa Ile Xaa Thr
        195   200   205

Tyr Asn Gly Asp Ser Phe Asp Xaa Pro Tyr Leu Xaa Lys Arg Ala Glu
    210   215   220

Lys Leu Gly Ile Lys Leu Xaa Xaa Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

Met Gln Arg Xaa Gly Asp Met Thr Ala Val Glu Xaa Lys Gly Arg Ile
            245   250   255

His Phe Asp Leu Tyr His Val Ile Xaa Arg Thr Ile Asn Leu Pro Thr
            260   265   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275   280   285

Lys Val Tyr Ala Xaa Glu Ile Ala Xaa Ala Trp Glu Xaa Gly Xaa Xaa
    290   295   300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Xaa Thr Tyr
305   310   315   320

Glu Leu Gly Xaa Glu Phe Xaa Pro Met Glu Xaa Gln Leu Ser Arg Leu
            325   330   335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340   345   350

Val Glu Trp Xaa Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Xaa Ala
        355   360   365

Pro Asn Lys Pro Xaa Glu Xaa Glu Tyr Xaa Arg Arg Leu Arg Glu Ser
    370   375   380

Tyr Xaa Gly Gly Xaa Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Xaa
385   390   395   400

Xaa Val Xaa Leu Asp Phe Arg Xaa Leu Tyr Pro Ser Ile Ile Ile Thr
            405   410   415

His Asn Val Ser Pro Asp Thr Leu Asn Xaa Glu Gly Cys Xaa Xaa Tyr
            420   425   430

Asp Xaa Ala Pro Xaa Val Gly His Lys Phe Cys Lys Asp Xaa Pro Gly
        435   440   445

45

Phe Ile Pro Ser Leu Leu Xaa Xaa Leu Leu Xaa Glu Arg Gln Xaa Ile
    450   455   460

Lys Xaa Lys Met Lys Xaa Xaa Xaa Asp Pro Ile Glu Lys Xaa Xaa Leu
465   470   475   480

Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly
            485   490   495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500   505   510

Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu
        515   520   525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530   535   540

Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Xaa Glu Glu Ile Lys Lys Lys
545   550   555   560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Xaa Lys Leu Pro Gly Leu Leu
            565   570   575

Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly Phe Phe Val Thr Lys
        580   585   590

Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys Xaa Ile Thr Arg Gly
    595   600   605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610   615   620

Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly Xaa Val Glu Glu Ala
625   630   635   640

Val Xaa Ile Val Lys Glu Val Xaa Xaa Lys Leu Xaa Xaa Tyr Glu Ile
            645   650   655

Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
.   660   665   670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Xaa Leu Ala
        675   680   685

Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val Ile Gly Tyr Ile Val
    690   695   700

Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala Ile Leu Ala Glu Glu
705   710   715   720

Xaa Asp Xaa Xaa Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725   730   735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Xaa Phe Gly Tyr Arg
            740   745   750

46

```
Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln Xaa Gly Leu Thr Xaa
        755                 760                 765

Trp Leu Asn Ile Lys Lys Ser
    770             775


<210> 27
<211> 783
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:designed hybrid
      polymerase from Figure 1

<220>
<221> MOD_RES
<222> (1)..(783)
<223> Xaa = unknown amino acid

<400> 27
Met Ile Leu Asp Xaa Asp Tyr Ile Thr Glu Xaa Gly Lys Pro Xaa Ile
 1               5               10                  15

Arg Xaa Phe Lys Lys Glu Asn Gly Xaa Phe Lys Xaa Glu Xaa Asp Arg
        20              25                  30

Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile
        35              40                  45

Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg
    50              55                  60

Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile
 65                 70                  75                  80

Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile
                85              90                  95

Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr
        100             105                 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115             120                 125

Met Glu Gly Xaa Glu Glu Leu Lys Xaa Leu Ala Phe Asp Ile Glu Thr
    130             135                 140

Leu Tyr His Glu Gly Glu Glu Phe Xaa Lys Gly Pro Ile Ile Met Ile
145             150             155                 160

Ser Tyr Ala Asp Glu Xaa Glu Ala Lys Val Ile Thr Trp Lys Xaa Ile
                165             170                 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
        180             185                 190

Arg Phe Leu Xaa Xaa Ile Arg Glu Lys Asp Pro Asp Xaa Ile Xaa Thr
        195             200                 205
```

47

```
Tyr Asn Gly Asp Ser Phe Asp Xaa Pro Tyr Leu Xaa Lys Arg Ala Glu
    210             215             220

Lys Leu Gly Ile Lys Leu Xaa Xaa Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235             240

Met Gln Arg Xaa Gly Asp Met Thr Ala Val Glu Xaa Lys Gly Arg Ile
            245             250             255

His Phe Asp Leu Tyr His Val Ile Xaa Arg Thr Ile Asn Leu Pro Thr
            260             265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275             280             285

Lys Val Tyr Ala Xaa Glu Ile Ala Xaa Ala Trp Glu Xaa Gly Xaa Xaa
    290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Xaa Thr Tyr
305             310             315             320

Glu Leu Gly Xaa Glu Phe Xaa Pro Met Glu Xaa Gln Leu Ser Arg Leu
            325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Xaa Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Xaa Ala
        355             360             365

Pro Asn Lys Pro Xaa Glu Xaa Glu Tyr Xaa Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Xaa Gly Gly Xaa Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Xaa
385             390             395             400

Xaa Val Xaa Leu Asp Phe Arg Xaa Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Xaa Glu Gly Cys Xaa Xaa Tyr
            420             425             430

Asp Xaa Ala Pro Xaa Val Gly His Lys Phe Cys Lys Asp Xaa Pro Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Xaa Xaa Leu Leu Xaa Glu Arg Gln Xaa Ile
    450             455             460

Lys Xaa Lys Met Lys Xaa Xaa Xaa Asp Pro Ile Glu Lys Xaa Xaa Leu
465             470             475             480

Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510

Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu
        515             520             525
```

48

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530   535   540

Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Xaa Glu Glu Ile Lys Lys Lys
545   550   555   560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Xaa Lys Leu Pro Gly Leu Leu
                565   570   575

Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly Phe Phe Val Thr Lys
                580   585   590

Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys Xaa Ile Thr Arg Gly
        595   600   605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610   615   620

Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly Xaa Val Glu Glu Ala
625   630   635   640

Val Xaa Ile Val Lys Glu Val Xaa Xaa Lys Leu Xaa Xaa Tyr Glu Ile
            645   650   655

Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660   665   670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Xaa Leu Ala
        675   680   685

Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val Ile Gly Tyr Ile Val
    690   695   700

Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala Ile Leu Ala Glu Glu
705   710   715   720

Xaa Asp Xaa Xaa Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725   730   735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Xaa Phe Gly Tyr Arg
            740   745   750

Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln Xaa Gly Leu Thr Xaa
        755   760   765

Trp Leu Asn Ile Lys Lys Ser Gly Thr His Asn Cys Asn His Asp
    770   775   780

<210> 28
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
     polymerase HyS1 from Figure 5

49

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 28
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile
 1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg
                20   25   30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
            35   40   45

Glu Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Val Asp Val Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
65   70   75   80

Lys Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
            85   90   95

Arg Asp Lys Val Arg Glu His Pro Ala Val Ile Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Ala Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Gly Ser Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
            165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180   185   190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
            195   200   205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210   215   220

Lys Leu Gly Ile Lys Leu Thr Leu Gly Arg Asp Gly Cys Glu Ala Lys
225   230   235   240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245   250   255

His Phe Asp Leu Tyr Tyr Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
            260   265   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
    275   280   285

50

```
Lys Val Tyr Ala Asp Asp Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
    290                 295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315                 320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ala Gln Leu Ser Arg Leu
            325             330                 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
        355             360             365

Pro Asn Lys Pro Tyr Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Ser
385             390             395                 400

Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420             425             430

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
    450             455             460

Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475                 480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545             550             555                 560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605
```

51

```
Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635                         640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645             650                     655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660             665                 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675             680             685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
705             710             715                         720

Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730                 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
        755             760             765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
770             775             780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785             790             795                         800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
            805             810             815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
        820             825             830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
        835             840             845


<210> 29
<211> 758
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Hyb2 from Figure 5

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid
```

52

<400> 29

```
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1               5                   10                  15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20                  25                  30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
        35                  40                  45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50                  55                  60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65                  70                  75                  80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
            85                  90                  95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
            100                 105                 110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115                 120                 125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130                 135                 140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145                 150                 155                 160

Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
            165                 170                 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
        180                 185                 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
        195                 200                 205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210                 215                 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225                 230                 235                 240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245                 250                 255

His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
        260                 265                 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275                 280                 285

Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
    290                 295                 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
305                 310                 315                 320
```

53

```
Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
            325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
        355             360             365

Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
385             390             395             400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420             425             430

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
    450             455             460

Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640
```

54

```
Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645                 650                 655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660                 665                 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675                 680                 685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690                 695                 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705                 710                 715                 720

Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725                 730                 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740                 745                 750

Lys Glu Asp Leu Arg Asn
        755


<210> 30
<211> 758
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Hyb3 from Figure 5

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 30
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1             5               10                  15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20              25                  30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
        35              40                  45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50                  55                  60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65                  70                  75                  80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
            85                  90                  95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
            100                 105                 110
```

```
Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115             120                 125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130             135                 140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145                 150                 155                     160

Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
            165                 170                 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180                 185                 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
        195                 200                 205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210                 215                 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225                 230                 235                     240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245                 250                 255

His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
            260                 265                 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275                 280                 285

Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
    290                 295                 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
305                 310                 315                     320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
            325                 330                 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340                 345                 350

Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
        355                 360                 365

Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370                 375                 380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
385                 390                 395                     400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405                 410                 415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420                 425                 430
```

56

```
Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
        450             455             460

Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475                     480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
                485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
            515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
        660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675             680             685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735
                                        .
```

57

```
Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740                 745                 750

Lys Glu Asp Leu Arg Asn
            755


<210> 31
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase HyS4 from Figure 5

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 31
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1             5                  10                  15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20                  25                  30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
            35                  40                  45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
        50                  55                  60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65                  70                  75                  80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
                85                  90                  95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
            100                 105                 110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115                 120                 125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
        130                 135                 140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145                 150                 155                 160

Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
                165                 170                 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180                 185                 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
            195                 200                 205
```

58

```
Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210             215             220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235             240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245             250             255

His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
            260             265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275             280             285

Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
    290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
305             310             315             320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
            325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
        355             360             365

Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
385             390             395             400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420             425             430

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
    450             455             460

Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        515             520             525
```

59

```
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530              535              540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545              550              555              560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
                 565              570              575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580              585              590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595              600              605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610              615              620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625              630              635              640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645              650              655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660              665              670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675              680              685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690              695              700

Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
705              710              715              720

Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725              730              735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740              745              750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
            755              760              765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val
    770              775              780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785              790              795              800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
                 805              810              815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
            820              825              830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
        835              840              845
```

60

<210> 32
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase PhS1 from Figure 5

<400> 32
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu His Asp Arg
                20   25   30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
            35   40   45

Glu Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65   70   75   80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
            85   90   95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115   120   125

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
            165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180   185   190

Arg Phe Leu Lys Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
            195   200   205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210   215   220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245   250   255

His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
            260   265   270

```
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275             280             285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Thr Gly Glu Gly
        290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315             320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
                325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
        355             360             365

Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Ala Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395             400

Ile Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Asn Tyr
            420             425             430

Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Lys Ile
    450             455             460

Lys Thr Lys Met Lys Ala Ser Gln Asp Pro Ile Glu Lys Ile Met Leu
465             470             475             480

Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
        580             585             590
```

62

Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595   600   605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610   615   620

Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625   630   635   640

Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ser Lys Tyr Glu Ile
            645   650   655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
        660   665   670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
        675   680   685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690   695   700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705   710   715   720

Tyr Asp Pro Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725   730   735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
        740   745   750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ser
        755   760   765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
    770   775   780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785   790   795   800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
            805   810   815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
            820   825   830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
        835   840   845

<210> 33
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase PhS2 from Figure 5

<400> 33
Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1   5   10   15

63

```
Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20              25              30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
        35              40              45

Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
    50              55              60

Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Lys Pro Ile
65              70              75              80

Glu Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
            85              90              95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
            100             105             110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115             120             125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
    130             135             140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145             150             155             160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
            165             170             175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
        180             185             190

Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
        195             200             205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
    210             215             220

Lys Leu Gly Ile Lys Leu Pro Ile Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235             240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245             250             255

His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
        260             265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275             280             285

Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Ser Gly Glu Gly
    290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315             320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ile Gln Leu Ser Arg Leu
            325             330             335
```

64

```
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
        355             360             365

Pro Asn Lys Pro Ser Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395             400

Ile Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Glu Tyr
            420             425             430

Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
    450             455             460

Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480

Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Arg Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Asp Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
        580             585             590

Lys Arg Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Thr Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
            645             650             655
```

65

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Pro Pro Leu His
            660   665   670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
            675   680   685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690   695   700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705   710   715   720

Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725   730   735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
            740   745   750

Lys Glu Asp Leu Arg Tyr Gln Lys Thr Lys Gln Val Asp Leu Thr Ala
            755   760   765

Cys Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
    770   775   780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785   790   795   800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
            805   810   815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
            820   825   830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
            835   840   845

<210> 34
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
     polymerase PhS3 from Figure 5

<400> 34
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Ile Ile
  1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Val Glu Tyr Asp Arg
            20   25   30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
            35   40   45

Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65   70   75   80

66

Glu Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
                85   90   95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
                100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
                115   120   125

Met Glu Gly Val Arg Tyr Arg Asn Pro Leu Ser Arg Arg Arg Arg Val
    130   135   140

Trp
145

<210> 35
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase PhS4 from Figure 5

<400> 35
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
    1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
                20   25   30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
            35   40   45

Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
        50   55   60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65   70   75   80

Glu Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Ala Ile
                85   90   95

Arg Glu Lys Val Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
                100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
                115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
                165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
                180   185   190

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Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
        195                 200                 205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Val Lys Arg Ala Glu
        210                 215                 220

Lys Leu Gly Ile Lys Leu Pro Ile Gly Arg Asp Gly Ser Glu Pro Lys
225                 230                 235                 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
                245                 250                 255

His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
                260                 265                 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275                 280                 285

Lys Val Tyr Ala His Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Gly
        290                 295                 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
305                 310                 315                 320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
                325                 330                 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
                340                 345                 350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
        355                 360                 365

Pro Asn Lys Pro Ser Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
        370                 375                 380

Tyr Ala Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385                 390                 395                 400

Ile Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
                405                 410                 415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asn Tyr
                420                 425                 430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
        435                 440                 445

Phe Ile Pro Ser Leu Leu Lys His Leu Leu Asp Glu Arg Gln Lys Ile
        450                 455                 460

Lys Arg Lys Met Lys Glu Ser Gln Asp Pro Ile Glu Lys Lys Met Leu
465                 470                 475                 480

Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
                485                 490                 495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
                500                 505                 510
```

```
Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu
        515                 520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Gly Leu
        530             535             540

Tyr Ala Thr Ile Pro Gly Ala Lys Ser Glu Glu Ile Lys Lys Lys Ala
545             550             555                     560

Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu Glu
                565             570             575

Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys
            580             585             590

Arg Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly Leu
        595             600             605

Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala
    610             615             620

Arg Val Leu Glu Thr Ile Leu Lys His Gly Asn Val Glu Glu Ala Val
625             630             635                     640

Arg Ile Val Lys Glu Val Thr Lys Lys Leu Ser Asn Tyr Glu Ile Pro
            645             650             655

Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu
        660             665             670

Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala
        675             680             685

Lys Gly Val Lys Ile Arg Pro Gly Met Val Ile Gly Tyr Ile Val Leu
    690             695             700

Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu Tyr
705             710             715                     720

Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln
            725             730             735

Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg Lys
            740             745             750

Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ala Trp
        755             760             765

Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val Lys
        770             775             780

Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys
785             790             795                     800

Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly
            805             810             815
```

69

Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys
            820   825   830

Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
            835   840

<210> 36
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase PhS5 from Figure 5

<400> 36
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
  1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20   25   30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
            35   40   45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
     50   55   60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65   70   75   80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
            85   90   95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
     130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
                165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180   185   190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
            195   200   205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
     210   215   220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

70

```
Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
            245             250             255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
            260             265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
            275             280             285

Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn
        290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315             320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
                325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
            355             360             365

Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
        370             375             380

Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395             400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr
            420             425             430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Lys His Leu Leu Asp Glu Arg Gln Glu Ile
    450             455             460

Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu
465             470             475             480

Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Trp Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Lys Pro Glu Glu Ile Lys Lys Lys
545             550             555             560
```

```
Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
              565             570         575

Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
              580             585         590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
              595             600         605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
              645             650         655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
              660             665         670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
              675         680             685

Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
              725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
              740             745         750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser
              755             760         765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val
    770             775             780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785             790             795             800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
                805             810             815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
              820             825             830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
          835             840             845


<210> 37
<211> 472
<212> PRT
<213> Artificial Sequence
```

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<220>
<223> Description of Artificial Sequence:hybrid
      polymerase PhS6 from Figure 5

<400> 37
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
 1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20   25   30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
            35   40   45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65   70   75   80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
            85   90   95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
            165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180   185   190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
            195   200   205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
    210   215   220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
            245   250   255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
            260   265   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
            275   280   285

Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn
    290   295   300

73

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305   310   315   320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
            325   330   335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340   345   350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
        355   360   365

Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370   375   380

Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385   390   395   400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405   410   415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr
            420   425   430

Asp Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
        435   440   445

Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Glu Glu Arg Gln Lys Ile
    450   455   460

Lys Arg Lys Met Lys Ala Thr Asn
465   470

<210> 38
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region
      containing invariable sequence element from
      parental Pfu polymerase containing nucleotide
      binding motif

<400> 38
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
 1   5   10   15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            20   25   30

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
        35   40   45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
    50   55   60

74

```
<210> 39
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region
      containing invariable sequence element from
      parental Deep Vent polymerase containing
      nucleotide binding motif

<400> 39
Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
  1               5                  10                  15


Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
              20                  25                  30


Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu
          35                  40                  45


Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
      50                  55                  60



<210> 40
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region
      containing invariable sequence element from
      dedigned hybrid polymerase containing nucleotide
      binding motif

<220>
<221> MOD_RES
<222> (1)..(60)
<223> Xaa = unknown amino acid

<400> 40
Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly
  1               5                  10                  15


Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
              20                  25                  30


Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu
          35                  40                  45


Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
      50                  55                  60



<210> 41
<211> 60
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:region
      containing invariable sequence elements from HyS1,
      Hyb2, Hyb3 and HyS4 hybrid polymerase containing
      nucleotide binding motif

<400> 41
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
 1   5   10   15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            20   25   30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        35   40   45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
        50   55   60

<210> 42
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region
      containing invariable sequence element from PhS1
      hybrid polymerase containing nucleotide binding
      motif

<400> 42
Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
 1   5   10   15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            20   25   30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        35   40   45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
        50   55   60

<210> 43
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region
      containing invariable sequence element from PhS2
      hybrid polymerase containing nucleotide binding
      motif

<400> 43
Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
 1   5   10   15

76

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
          20   25   30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Arg Lys Glu
          35   40   45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
     50   55   60

<210> 44
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region
      containing invariable sequence element from PhS4
      hybrid polymerase containing nucleotide binding
      motif

<400> 44
Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
 1   5   10   15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
          20   25   30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu
          35   40   45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
     50   55   60

<210> 45
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region
      containing invariable sequence element from PhS5
      hybrid polymerase containing nucleotide binding
      motif

<400> 45
Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
 1   5   10   15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
          20   25   30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Trp Lys Glu
          35   40   45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
     50   55   60

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<210> 46
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region
     containing invariable sequence element from PhS7
     hybrid polymerase containing nucleotide binding
     motif

<400> 46
Asp Tyr Arg Gln Lys Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly
 1               5                  10                  15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            20                  25                  30

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Phe Val Arg Lys Glu
        35                  40                  45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
    50                  55                  60


<210> 47
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:6-His
     polyhistidine epitope tag, metal chelate affinity
     ligand

<400> 47
His His His His His His
 1               5


<210> 48
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anti-DYKDDDDK
     epitope tag

<400> 48
Asp Tyr Lys Asp Asp Asp Asp Lys
 1               5


<210> 49
<211> 45
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:primer to
      measure exonuclease activity

<220>
<221> modified_base
<222> (1)
<223> n = t modified by 6-carboxy-fluorescein (FAM)

<220>
<221> modified_base
<222> (45)
<223> n = t amino-linked to quencher
      4-(4-dimethylaminophenylazo)benzoyl group (dabcyl,
      DAB)

<400> 49
nttttgagg tgtgtcctac acagcggagt gtaggacaca cctcn   45